R. Mitra

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RAW SEQUENCE LISTING DATE: 09/06/2001
PATENT APPLICATION: **US/09/687,276** TIME: 10:55:17

Input Set : **A:\Cura-851.app**
Output Set: **N:\CRF3\09062001\I687276.raw**

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 3 <110> APPLICANT: Prayaga, Sudhirdas K
 4       Taupier Jr, Raymond J
 5       Bandaru, Raj
 7 <120> TITLE OF INVENTION: NOVEL THYMOSIN BETA 10-LIKE PROTEINS AND NUCLEIC ACIDS
 8       ENCODING SAME
10 <130> FILE REFERENCE: 15966-585A
12 <140> CURRENT APPLICATION NUMBER: 09/687,276
13 <141> CURRENT FILING DATE: 2000-10-13
15 <150> PRIOR APPLICATION NUMBER: 60/159,805
16 <151> PRIOR FILING DATE: 1999-10-15
18 <150> PRIOR APPLICATION NUMBER: 60/159,992
19 <151> PRIOR FILING DATE: 1999-10-18
21 <150> PRIOR APPLICATION NUMBER: 60/160,952
22 <151> PRIOR FILING DATE: 1999-10-22
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40 atg gca gac aaa cca gac ata ggg gaa atc gcc agc ttc aat aag gcc   108
41 Met Ala Asp Lys Pro Asp Ile Gly Glu Ile Ala Ser Phe Asn Lys Ala
42   1               5                  10                  15
44 aag ctg aag aaa aca gag atg cag gag aac acc ctg ctg acc aaa gag   156
45 Lys Leu Lys Lys Thr Glu Met Gln Glu Asn Thr Leu Leu Thr Lys Glu
46             20                  25                  30
48 gcc att gag cag gag aag cgg gtg aaa ttt cct aag agc ctg gag gat   204
49 Ala Ile Glu Gln Glu Lys Arg Val Lys Phe Pro Lys Ser Leu Glu Asp
50          35                  40                  45
52 tcc cta ccc ctg tca tct tcg aga ccc cag tagtaatgtg gaggaagaat     254
53 Ser Leu Pro Leu Ser Ser Ser Arg Pro Gln
54      50                  55
56 caccacaaga tggacacaag ccacaaactg tgacgtgaac ctgggcactc cgtgctgatg 314
58 ccaccagcct gagggtccct atgggtccaa tcagactgcc aaattctctg gtttgccctg 374
60 ggatattata gaaaattatt tgcgtgaata atgaaaacac agctcatggc aaaaaa     430
63 <210> SEQ ID NO: 2
64 <211> LENGTH: 58
65 <212> TYPE: PRT
66 <213> ORGANISM: Homo sapiens
68 <400> SEQUENCE: 2
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70   1               5                  10                  15
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72 Lys Leu Lys Lys Thr Glu Met Gln Glu Asn Thr Leu Leu Thr Lys Glu
73 20 25 30
75 Ala Ile Glu Gln Glu Lys Arg Val Lys Phe Pro Lys Ser Leu Glu Asp
76 35 40 45
78 Ser Leu Pro Leu Ser Ser Ser Arg Pro Gln
79 50 55
83 <210> SEQ ID NO: 3
84 <211> LENGTH: 13
85 <212> TYPE: PRT
86 <213> ORGANISM: Homo sapiens
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90 1 5 10
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101 cacggggact ggggctggct cacgtatccg gctcatgggt gggactccat caacgaggtg 180
102 gacgagtcct tccagcccat ccacacgtac caggtttgca acgtcatgag ccccaaccag 240
103 aacaactggc tgcgcacgag ctgggtcccc cgagacggcg cccggcgcgt ctatgctgag 300
104 atcaagttta ccctgcgcga ctgcaacagc atgcctggtg tgctgggcac ctgcaaggag 360
105 accttcaacc tctactacct ggagtcggac cgcgacctgg gggccagcac acaagaaagc 420
106 cagttcctca aaatcgacac cattgcggcc gacgagagct tcacaggtgc cgaccttggt 480
107 gtgcggcgtc tcaagctcaa cacggaggtg cgcagtgtgg gtcccctcag caagcgcggc 540
108 ttctacctgg ccttccagga cataggtgcc tgcctggcca tcctctctct ccgcatctac 600
109 tataagaagt gccctgccat ggtgcgcaat ctggctgcct tctcggaggc agtgacgggg 660
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123 gacaaggaga tgcagagcta ctccaccctc aaggccgtca ccaccagagc caccgtctcc 1500
124 ggcctcaagc cgggcacccg ctacgtgttc caggtccgag cccgcacctc agcaggctgt 1560
125 ggccgcttca gccaggccat ggaggtggag accgggaaac cccggccccg ctatgacacc 1620
126 aggaccattg tctggatctg cctgacgctc atcacgggcc tggtggtgct tctgctcctg 1680
127 ctcatctgca agaagaggca ctgtggctac agcaaggcct tccaggactc ggacgaggag 1740
128 aagatgcact atcagaatgg acaggcaccc ccacctgtct tcctgcctct gcatcacccc 1800
129 ccgggaaagc tcccagagcc ccagttctat gcggaacccc acacctacga ggagccaggc 1860

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132 gatgtgcccg tggccatcaa ggccctcaaa gccggctaca cggagagaca gaggcgggac 2040
133 ttcctgagcg aggcgtccat catggggcaa ttcgaccatc ccaacatcat ccgcctcgag 2100
134 ggtgtcgtca cccgtggccg cctggcaatg attgtgactg agtacatgga gaacggctct 2160
135 ctggacacct tcctgaggac ccacgacggg cagttcacca tcatgcagct ggtgggcatg 2220
136 ctgagaggag tgggtgccgg catgcgctac ctctcagacc tgggctatgt ccaccgagac 2280
137 ctggccgccc gcaacgtcct ggttgacagc aacctggtct gcaaggtgtc tgacttcggg 2340
138 ctctcacggg tgctggagga cgacccggat gctgcctaca ccaccacggg cgggaagatc 2400
139 cccatccgct ggacggcccc agaggccatc gccttccgca ccttctcctc ggccagcgac 2460
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141 aacatgacca accgggatgt gatcagctct gtggaggagg ggtaccgcct gcccgcaccc 2580
142 atgggctgcc cccacgccct gcaccagctc atgctcgact gttggcacaa ggaccgggcg 2640
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145 tttgacctcc gaggggggcag cggtggcggt gggggcctca ccgtggggga ctggctggac 2820
146 tccatccgca tgggccggta ccgagaccac ttcgctgcgg gcggatactc ctctctgggc 2880
147 atggtgctac gcatgaacgc ccaggacgtg cgcgccctgg gcatcaccct catgggccac 2940
148 cagaagaaga tcctgggcag cattcagacc atgcgggccc agctgaccag cacccagggg 3000
149 ccccgccggc acctctga                                              3018
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153 <211> LENGTH: 992
154 <212> TYPE: PRT
155 <213> ORGANISM: Homo sapiens
157 <400> SEQUENCE: 5
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162              20                  25                  30
164 Asn Leu Leu Asp Thr Ser Thr Ile His Gly Asp Trp Gly Trp Leu Thr
165          35                  40                  45
167 Tyr Pro Ala His Gly Trp Asp Ser Ile Asn Glu Val Asp Glu Ser Phe
168      50                  55                  60
170 Gln Pro Ile His Thr Tyr Gln Val Cys Asn Val Met Ser Pro Asn Gln
171  65                  70                  75                  80
173 Asn Asn Trp Leu Arg Thr Ser Trp Val Pro Arg Asp Gly Ala Arg Arg
174                  85                  90                  95
176 Val Tyr Ala Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Met Pro
177              100                 105                 110
179 Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Leu Glu
180          115                 120                 125
182 Ser Asp Arg Asp Leu Gly Ala Ser Thr Gln Glu Ser Gln Phe Leu Lys
183      130                 135                 140
185 Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gly Ala Asp Leu Gly
186 145                 150                 155                 160
188 Val Arg Arg Leu Lys Leu Asn Thr Glu Val Arg Ser Val Gly Pro Leu
189                 165                 170                 175
191 Ser Lys Arg Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala Cys Leu
192              180                 185                 190
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194 Ala Ile Leu Ser Leu Arg Ile Tyr Tyr Lys Lys Cys Pro Ala Met Val
195         195                 200                 205
197 Arg Asn Leu Ala Ala Phe Ser Glu Ala Val Thr Gly Ala Asp Ser Ser
198     210                 215                 220
200 Ser Leu Val Glu Val Arg Gly Gln Cys Val Arg His Ser Glu Glu Arg
201 225                 230                 235                 240
203 Asp Thr Pro Lys Met Tyr Cys Ser Ala Glu Gly Glu Trp Leu Val Pro
204                 245                 250                 255
206 Ile Gly Lys Cys Val Cys Ser Ala Gly Tyr Glu Glu Arg Arg Asp Ala
207             260                 265                 270
209 Cys Val Ala Cys Glu Leu Gly Phe Tyr Lys Ser Ala Pro Gly Asp Gln
210         275                 280                 285
212 Leu Cys Ala Arg Cys Pro Pro His Ser His Ser Ala Ala Pro Ala Ala
213     290                 295                 300
215 Gln Ala Cys His Cys Asp Leu Ser Tyr Tyr Arg Ala Ala Leu Asp Pro
216 305                 310                 315                 320
218 Pro Ser Ser Ala Cys Thr Arg Pro Pro Ser Ala Pro Val Asn Leu Ile
219                 325                 330                 335
221 Ser Ser Val Asn Gly Thr Ser Val Thr Leu Glu Trp Ala Pro Pro Leu
222             340                 345                 350
224 Asp Pro Gly Gly Arg Ser Asp Ile Thr Tyr Asn Ala Val Cys Arg Arg
225         355                 360                 365
227 Cys Pro Trp Ala Leu Ser Arg Cys Glu Ala Cys Gly Ser Gly Thr Arg
228     370                 375                 380
230 Phe Val Pro Gln Gln Thr Ser Leu Val Gln Ala Ser Leu Leu Val Ala
231 385                 390                 395                 400
233 Asn Leu Leu Ala His Met Asn Tyr Ser Phe Trp Ile Glu Ala Val Asn
234                 405                 410                 415
236 Gly Val Ser Asp Leu Ser Pro Glu Pro Arg Arg Ala Ala Val Val Asn
237             420                 425                 430
239 Ile Thr Thr Asn Gln Ala Ala Pro Ser Gln Val Val Val Ile Arg Gln
240         435                 440                 445
242 Glu Arg Ala Gly Gln Thr Ser Val Ser Leu Leu Trp Gln Glu Pro Glu
243     450                 455                 460
245 Gln Pro Asn Gly Ile Ile Leu Glu Tyr Glu Ile Lys Tyr Tyr Glu Lys
246 465                 470                 475                 480
248 Asp Lys Glu Met Gln Ser Tyr Ser Thr Leu Lys Ala Val Thr Thr Arg
249                 485                 490                 495
251 Ala Thr Val Ser Gly Leu Lys Pro Gly Thr Arg Tyr Val Phe Gln Val
252             500                 505                 510
254 Arg Ala Arg Thr Ser Ala Gly Cys Gly Arg Phe Ser Gln Ala Met Glu
255         515                 520                 525
257 Val Glu Thr Gly Lys Pro Arg Pro Arg Tyr Asp Thr Arg Thr Ile Val
258     530                 535                 540
260 Trp Ile Cys Leu Thr Leu Ile Thr Gly Leu Val Val Leu Leu Leu Leu
261 545                 550                 555                 560
263 Leu Ile Cys Lys Lys Arg His Cys Gly Tyr Ser Lys Ala Phe Gln Asp
264                 565                 570                 575
266 Ser Asp Glu Glu Lys Met His Tyr Gln Asn Gly Gln Ala Pro Pro Pro
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267                 580                 585                 590
269 Val Phe Leu Pro Leu His His Pro Pro Gly Lys Leu Pro Glu Pro Gln
270         595                 600                 605
272 Phe Tyr Ala Glu Pro His Thr Tyr Glu Glu Pro Gly Arg Ala Gly Arg
273     610                 615                 620
275 Ser Phe Thr Arg Glu Ile Glu Ala Ser Arg Ile His Ile Glu Lys Ile
276 625                 630                 635                 640
278 Ile Gly Ser Gly Asp Ser Gly Glu Val Cys Tyr Gly Arg Leu Arg Val
279                 645                 650                 655
281 Pro Gly Gln Arg Asp Val Pro Val Ala Ile Lys Ala Leu Lys Ala Gly
282                 660                 665                 670
284 Tyr Thr Glu Arg Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile Met
285         675                 680                 685
287 Gly Gln Phe Asp His Pro Asn Ile Ile Arg Leu Glu Gly Val Val Thr
288     690                 695                 700
290 Arg Gly Arg Leu Ala Met Ile Val Thr Glu Tyr Met Glu Asn Gly Ser
291 705                 710                 715                 720
293 Leu Asp Thr Phe Leu Arg Thr His Asp Gly Gln Phe Thr Ile Met Gln
294                 725                 730                 735
296 Leu Val Gly Met Leu Arg Gly Val Gly Ala Gly Met Arg Tyr Leu Ser
297                 740                 745                 750
299 Asp Leu Gly Tyr Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val
300         755                 760                 765
302 Asp Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val
303     770                 775                 780
305 Leu Glu Asp Asp Pro Asp Ala Ala Tyr Thr Thr Thr Gly Gly Lys Ile
306 785                 790                 795                 800
308 Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Phe Arg Thr Phe Ser
309                 805                 810                 815
311 Ser Ala Ser Asp Val Trp Ser Phe Gly Val Val Met Trp Glu Val Leu
312                 820                 825                 830
314 Ala Tyr Gly Glu Arg Pro Tyr Trp Asn Met Thr Asn Arg Asp Val Ile
315         835                 840                 845
317 Ser Ser Val Glu Glu Gly Tyr Arg Leu Pro Ala Pro Met Gly Cys Pro
318     850                 855                 860
320 His Ala Leu His Gln Leu Met Leu Asp Cys Trp His Lys Asp Arg Ala
321 865                 870                 875                 880
323 Gln Arg Pro Arg Phe Ser Gln Ile Val Ser Val Leu Asp Ala Leu Ile
324                 885                 890                 895
326 Arg Ser Pro Glu Ser Leu Arg Ala Thr Ala Thr Val Ser Arg Cys Pro
327                 900                 905                 910
329 Pro Pro Ala Phe Val Arg Ser Cys Phe Asp Leu Arg Gly Gly Ser Gly
330         915                 920                 925
332 Gly Gly Gly Gly Leu Thr Val Gly Asp Trp Leu Asp Ser Ile Arg Met
333     930                 935                 940
335 Gly Arg Tyr Arg Asp His Phe Ala Ala Gly Gly Tyr Ser Ser Leu Gly
336 945                 950                 955                 960
338 Met Val Leu Arg Met Asn Ala Gln Asp Val Arg Ala Leu Gly Ile Thr
339                 965                 970                 975
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